Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of claims:

Claim 1. (original) A method of identifying a nucleic acid molecule suitable for use in a probe for detecting the presence of one or more of a family of nucleic acid molecules, comprising the steps of:

(a) providing the family of first nucleic acid molecules wherein each member of the family is related to all other members of the family by consensus sequence;

(b) providing a second nucleic acid molecule having a sequence complementary to the consensus sequence;

(c) determining the ability of the second nucleic acid molecule to form a duplex with each member of the family in the presence of a first ligand known to affect duplex formation of nucleic acid molecules;

(d) repeating step (c) for a plurality of concentrations of the ligand, wherein the nucleic acid molecule suitable for use in a probe is identified in step (c) at a ligand concentration at which the ability of the second nucleic acid molecule to form a duplex with each member of the family is substantially the same as its ability to form a duplex with each other member of the family.

Claim 2. (original) The method of claim 1, further comprising the step of (e) repeating steps (c) and (d) for a second ligand.

Claim 3. (original) The method of claim 2, further comprising the step of (f) repeating steps (c) and (d) in the presence of both first and second ligands.

Claim 4. (original) The method of claim 3 wherein step (e) is repeated for each of a plurality of the second ligands and step (f) is repeated for each of the second ligands or combinations thereof.

Claim 5. (original) The method of claim 1, further comprising the step of (g) determining the percent homology of the second nucleic acid sequence against a plurality of nucleic acid sequences in a database prior to step (c), wherein the second nucleic acid sequence is less than a predetermined homology to other non-target partially complementary nucleic acid sequences.

Claim 6. (original) The method of claim 1, wherein the first and second ligands are selected from the group consisting of actinomycin D, distamycin A, diminazane aceturate, bisbenzimide, and ethidium bromide.

Claim 7. (original) The method of claim 1, wherein said first nucleic acid molecules of the family are at least a% homologous with each other, a being a number greater than 0 and less than 100, comprising the further steps of:

(i) providing a third nucleic acid molecule which is no more than b% homologous with each of the first nucleic acid molecules of the family, where b is a number greater than 0 and less than a;

(ii) repeating steps (c) and (d) in the presence of the third nucleic acid molecule so as to:

A. determine the ability of the second nucleic molecule and isthe third nucleic molecule to form a duplex with each other, and

B. determine a ligand concentration at which the ability of the second nucleic acid molecule to form a duplex with the third nucleic acid molecule is substantially different from the ability of the second nucleic acid molecule to form a duplex with each other member of the family, wherein the second nucleic acid molecule is suitable for use as a probe when the ligand concentration at which the ability of the second nucleic acid molecule to form a duplex with the third nucleic acid molecule is substantially different from the ability of the second nucleic acid molecule to form a duplex with each other member of the family and the ligand concentration at which the ability of the second nucleic acid molecule to form a duplex with each member of the family is substantially the same as

its ability to form a duplex with each other member of the family are substantially equal to each other.

Claim 8. (original) The method of claim 7 wherein the second nucleic acid molecule is suitable for use as a probe when the ligand concentration at which the ability of the second nucleic acid molecule to form a duplex with the third nucleic acid molecule is substantially less than the ability of the second nucleic acid molecule to form a duplex with each other member of the family and the ligand concentration at which the ability of the second nucleic acid molecule to form a duplex with each member of the family is substantially the same as its ability to form a duplex with each other member of the family are substantially equal to each other.

Claim 9. (original) The method of claim 7, further comprising the step of (e) repeating steps (c), (d), (i) and (ii) for a second ligand.

Claim 10. (original) The method of claim 9, further comprising the steps of (c), (d), (i) and (ii) in the presence of both the first and second ligands.

Claim 11. (original) The method of claim 1 wherein each of the first nucleic acid molecules is selected from a group consisting of a genetic sequence of a first virus and variants thereof known to exist in nature.

Claim 12. (original) The method of claim 7 wherein each of the nucleic acid sequences of the first nucleic acid molecules is selected from a genetic sequence of a first virus and variants thereof, and the nucleic acid sequence of the third nucleic acid molecule is selected from a group of genetic sequences known to exist in nature exclusive of the first virus and the variants.

Claim 13 (cancelled)

Claim 14. (original) A method of detecting the presence of a nucleic acid molecule suspected of being in a sample containing genetic material, the method comprising:

(a) providing the sample which contains or possibly contains a nucleic acid molecule which is a member of a family of first nucleic acid molecules that is related to all other members of the family by a consensus sequence;

(b) exposing the sample to a probe comprising a nucleotide sequence having a sequence complementary to the consensus sequence and identified according to the method of claim 1 as suitable for use in a probe, under conditions suitable for hybridization, in the presence of the ligand of claim 1 present at the concentration at which the ability of the second nucleic acid molecule to form a duplex with each member of the family is substantially the same as its ability to form a duplex with each other member of the family; and

(c) ascertaining whether any duplexed nucleic acid molecules comprising the probe formed in step (C), wherein the formation of the duplexed nucleic acid molecules indicates the presence of the nucleic acid molecule suspected of being in the sample.

Claim 15. (original) The method of claim 14, comprising the further step of exposing the same of to conditions suitable for amplifying the duplex formed in step (B).

Claim 16. (original) A method of promoting the hybridization of a nucleic acid capture moiety to a target single-stranded nucleic acid sequence and all its family members without hybridizing to a plurality of other non-target partially complementary nucleic acid sequences present in a sample, the steps comprising:

(a) providing:

(i) a nucleic acid capture moiety comprising the nucleic acid molecule identified in claim 5;

(ii) the sample containing the target duplex nucleic acid sequence or any of its family members, wherein the sample has been treated such that all duplex nucleic acid sequences present in the sample including the target duplex nucleic acid sequence and all its family members suspected of being present in the sample will denature and form single-stranded nucleic acid sequences; and

(iii) a nucleic acid sequence binding ligand;

(b) forming a reaction mixture comprising the nucleic acid capture moiety, the sample and binding ligand of steps (a)(i), (a)(ii) and (a)(iii), respectively under conditions such that the nucleic acid sequence binding ligand promotes hybridization of the target single-stranded nucleic acid sequence and all its family members to the nucleic acid capture moiety comprising the probe nucleic acid sequence identified in step (a) and not to other non-target partially complementary nucleic acid sequences;

(c) allowing the target single-stranded nucleic acid sequence and all its family members suspected of being present in a sample to hybridize to the nucleic acid capture moiety comprising the probe nucleic acid sequence identified in step (a) such that the nucleic acid sequence binding ligand promotes hybridization of the target single-stranded nucleic acid sequence and all its family members to the nucleic acid capture moiety comprising the probe nucleic acid sequence identified in step (a) without promoting the hybridization of other non-target partially complementary nucleic acid sequences; and

(d) detecting the presence or absence of the target single-stranded nucleic acid sequence and all its family members hybridized to the nucleic acid capture moiety.

Claim 17. (original) A method of promoting the hybridization of a nucleic acid capture moiety to a target single-stranded nucleic acid sequence and all its family members without hybridizing to a plurality of other non-target partially complementary nucleic acid sequences contained in a sample, the steps comprising:

(a) identifying at least one nucleic acid sequence probe substantially complementary to the target duplex nucleic acid sequence and all its family members suspected of being present in a sample and coupling at least one probe nucleic acid sequence with a label;

(b) identifying at least two substantially complementary primer nucleic acid sequences immediately 5' and 3' of the region of the target nucleic acid sequence and all its family members to be detected;

(c) treating the sample suspected of containing the target duplex nucleic acid sequences and all its family members with the two substantially complementary primer nucleic acid sequences in step (b), an agent for polymerization, and four nucleoside

triphosphates under conditions which allow amplification of the nucleic acid sequence to be detected thereof without simultaneous amplification of non-target partially complementary nucleic acid sequences from other viral nucleic acid sequences or human genomic nucleic acid sequences;

(d) treating the sample such that all duplex nucleic acid sequences present in the sample including the amplified target duplex nucleic acid sequence and all its family members suspected of being present in the sample denature and form single-stranded nucleic acid sequences;

(e) providing:

(i) a nucleic acid capture moiety comprising the labeled probe nucleic acid sequence identified in claim 5;

(ii) the sample suspected of containing the amplified single-stranded target nucleic acid sequence and all its family members; and

(iii) a nucleic acid sequence binding ligand;

(f) forming a reaction mixture comprising:

(i) the nucleic acid capture moiety comprising the labeled probe nucleic acid sequence identified in claim 5;

(ii) the sample suspected of containing the amplified single-stranded target nucleic acid sequence and all its family members; and

(iii) a nucleic acid sequence binding ligand;

under conditions such that the nucleic acid sequence binding ligand promotes hybridization of the amplified target single-stranded nucleic acid sequence and all its family members to the nucleic acid capture moiety comprising the probe nucleic acid sequence identified in step (a) and not to other non-target partially complementary nucleic acid sequences;

(g) allowing the amplified target single-stranded nucleic acid sequence and all its family members suspected of being present in a sample to hybridize to nucleic acid capture moiety comprising the probe nucleic acid sequence identified in step (a) such that the nucleic acid sequence binding ligand promotes hybridization of the target single-stranded nucleic acid sequence and all its family members to the nucleic acid capture moiety comprising the probe nucleic acid sequence identified in step (a) without

promoting the hybridization of other non-target partially complementary nucleic acid sequences; and

(h) detecting the presence or absence of the target single-stranded nucleic acid sequence and all its family members hybridized to the nucleic acid capture moiety.

Claim 18 (cancelled)

Claim 19. (original) The method of claim 17 wherein the nucleic acid sequence binding ligand is selected from the group consisting of: a compound which binds to a duplex nucleic acid in a sequence-specific way; a compound which binds to a duplex nucleic acid in a non-specific way; a protein; an enzyme; an enzyme which alters the structure of a duplex nucleic acid to which it binds; an enzyme which alters the structure of a duplex nucleic acid to which it binds by breaking or forming a covalent or non-covalent bond, between an atom of the nucleic acid and another atom; an enzyme which cleaves one or both strands of a duplex nucleic acid to which it binds; a restriction enzyme; a restriction endonuclease; an enzyme which methylates the duplex to which it binds; an enzyme which alkylates the duplex nucleic acid to which it binds; a nucleic acid ligase such as DNA ligase, an enzyme which promotes or catalyzes the synthesis of nucleic acid; a nucleic acid polymerase; a nucleic acid polymerase which requires a double stranded primer; a DNA polymerase; DNA polymerase I; Taq polymerase; an RNA polymerase; an enzyme which alters the primary or secondary structure of a duplex nucleic acid to which it binds; a topoisomerase; an enzyme which promotes or inhibits recombination; a DNA binding agent; a mutagen; a compound which enhances the expression of a gene under the control of the duplex bound by a ligand; a compound which interrelates into a duplex nucleic acid molecule; a compound which, when contacted with a reaction mixture comprising a first single stranded nucleic acid molecule and a second single stranded nucleic acid molecule will increase the free energy of duplex formation at least n-fold, wherein n is 2, 5,10, 50,100, 500,103,104, 105,106, a compound which, when contacted with a reaction mixture will decrease the free energy of duplex formation by at least n-fold, wherein n is 2, 5, 10, 50,100, 500, 103, 104, 105, 106.

Claim 20 (cancelled)

Claim 21. (original) The method of claim 19, wherein the nucleic acid sequence binding ligand further comprises a single-stranded nucleic acid binding ligand.

Claim 22. (original) The method of claim 19, wherein the nucleic acid sequence binding ligand further comprises a duplex nucleic acid sequence binding ligand.

Claim 23. (original) The method of claim 19, wherein the nucleic acid sequence binding ligand further comprises a nonspecific nucleic acid binding ligand.

Claim 24. (original) The method of claim 19, wherein the duplex nucleic acid sequence binding ligand is selected from the group consisting of actinomycin D, distamycin A, diminazene aceturate, bisbenzamide, and ethidium bromide.

Claims 25 to 29 (cancelled).

Claim 30. (original) The hybridization mixture of claim 18, wherein the nucleic acid capture moiety
comprises a structure A-B-C-D wherein:

A is a single-stranded nucleic acid sequence having a composition substantially complementary to a region of the target nucleic acid sequence and all its family members to be detected;

B and D are nucleic acid sequences which are capable of hybridizing to each other to form an intramolecular duplex; and

C is a linker which covalently links B and D.

31 (cancelled)

Claim 32. (original) The hybridization mixture of claim 19, wherein the label of the labeled probe nucleic acid sequence is selected from the group consisting of antibody, antigen, radioisotope, fluorescent, enzyme, lectin or biotin.

Claim 33. (original) A kit for detecting the presence of a target nucleic acid sequence and all its family members suspected of being present in a sample, the kit comprising:

(a) a nucleic acid capture moiety comprising a labeled probe nucleic acid sequence substantially complementary to the target duplex nucleic acid sequence and all its family members suspected of being present in a sample; and

(b) at least one nucleic acid sequence binding ligand, wherein the ligand can promote hybridization of the target single-stranded nucleic acid sequence and all its family members to the nucleic acid capture moiety and not to other non-target partially complementary nucleic acid sequences.

Claims 34 to 39 (cancelled)

Claim 40. (original) The method of claim 17 wherein the target nucleic acid sequence and all its family members to be detected is a region of a viral nucleic acid sequence and all its family members.

Claim 41. (original) The method of claim 40, wherein the region of viral nucleic acid to be detected is a region of the AIDS virus and all its family members.

Claim 42. (original) The method of claim 17, wherein the target nucleic acid sequence and all its family members to be detected is a region of an oncogene.

Claim 43. (original) The method of claim 47, wherein the oncogene is selected from the group consisting of p53, ras, BRCA1, or BRCA2 and each of their family members.

Claims 44 to 46 (cancelled)